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# 2

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/879,401A

DATE: 01/09/2003

TIME: 07:48:08

Input Set : N:\Crif3\RULE60\09879401.raw.txt

Output Set: N:\CRF4\01092003\I879401A.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:  
5 (i) APPLICANT: Lal, Preeti  
6 Hillman, Jennifer  
7 Corley, Neil  
8 Shah, Purvi  
10 (ii) TITLE OF INVENTION: HUMAN PHOSPHOLIPID BINDING PROTEINS  
12 (iii) NUMBER OF SEQUENCES: 6  
14 (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
16 (B) STREET: 3174 Porter Dr.  
17 (C) CITY: Palo Alto  
18 (D) STATE: CA  
19 (E) COUNTRY: USA  
20 (F) ZIP: 94304  
22 (v) COMPUTER READABLE FORM:  
23 (A) MEDIUM TYPE: Diskette  
24 (B) COMPUTER: IBM Compatible  
25 (C) OPERATING SYSTEM: DOS  
26 (D) SOFTWARE: FastSEQ for Windows Version 2.0  
28 (vi) CURRENT APPLICATION DATA:  
C--> 29 (A) APPLICATION NUMBER: US/09/879,401A  
C--> 30 (B) FILING DATE: 13-Jun-2001  
31 (C) CLASSIFICATION:  
33 (vii) PRIOR APPLICATION DATA:  
34 (A) APPLICATION NUMBER: US/08/958,820  
35 (B) FILING DATE: Filed Herewith  
38 (viii) ATTORNEY/AGENT INFORMATION:  
39 (A) NAME: Billings, Lucy J.  
40 (B) REGISTRATION NUMBER: 36,749  
41 (C) REFERENCE/DOCKET NUMBER: PF-0379 US  
43 (ix) TELECOMMUNICATION INFORMATION:  
44 (A) TELEPHONE: 650-855-0555  
45 (B) TELEFAX: 650-845-4166  
48 (2) INFORMATION FOR SEQ ID NO: 1:  
50 (i) SEQUENCE CHARACTERISTICS:  
51 (A) LENGTH: 214 amino acids  
52 (B) TYPE: amino acid  
53 (C) STRANDEDNESS: single  
54 (D) TOPOLOGY: linear  
56 (vii) IMMEDIATE SOURCE:  
57 (A) LIBRARY: MUSCNOT07  
58 (B) CLONE: 3014759

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62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

64	Met	Glu	Leu	Ala	Ala	Gly	Ser	Phe	Ser	Glu	Glu	Gln	Phe	Trp	Glu	Ala
65	1				5					10					15	
66	Cys	Ala	Glu	Leu	Gln	Gln	Pro	Ala	Leu	Ala	Gly	Ala	Asp	Trp	Gln	Leu
67				20					25					30		
68	Leu	Val	Glu	Thr	Ser	Gly	Ile	Ser	Ile	Tyr	Arg	Leu	Leu	Asp	Lys	Lys
69			35					40					45			
70	Thr	Gly	Leu	Tyr	Glu	Tyr	Lys	Val	Phe	Gly	Val	Leu	Glu	Asp	Cys	Ser
71		50					55					60				
72	Pro	Thr	Leu	Leu	Ala	Asp	Ile	Tyr	Met	Asp	Ser	Asp	Tyr	Arg	Lys	Gln
73	65				70					75					80	
74	Trp	Asp	Gln	Tyr	Val	Lys	Glu	Leu	Tyr	Glu	Gln	Glu	Cys	Asn	Gly	Glu
75				85					90						95	
76	Thr	Val	Val	Tyr	Trp	Glu	Val	Lys	Tyr	Pro	Phe	Pro	Met	Ser	Asn	Arg
77			100					105						110		
78	Asp	Tyr	Val	Tyr	Leu	Arg	Gln	Arg	Arg	Asp	Leu	Asp	Met	Glu	Gly	Arg
79			115				120					125				
80	Lys	Ile	His	Val	Ile	Leu	Ala	Arg	Ser	Thr	Ser	Met	Pro	Gln	Leu	Gly
81		130				135						140				
82	Glu	Arg	Ser	Gly	Val	Ile	Arg	Val	Lys	Gln	Tyr	Lys	Gln	Ser	Leu	Ala
83	145				150					155					160	
84	Ile	Glu	Ser	Asp	Gly	Lys	Lys	Gly	Ser	Lys	Val	Phe	Met	Tyr	Tyr	Phe
85			165					170						175		
86	Asp	Asn	Pro	Gly	Gly	Gln	Ile	Pro	Ser	Trp	Leu	Ile	Asn	Trp	Ala	Ala
87			180					185						190		
88	Lys	Asn	Gly	Val	Pro	Asn	Phe	Leu	Lys	Asp	Met	Ala	Arg	Ala	Cys	Gln
89		195				200						205				
90	Asn	Tyr	Leu	Lys	Lys	Thr										
91		210														

93 (2) INFORMATION FOR SEQ ID NO: 2:

95 (i) SEQUENCE CHARACTERISTICS:

96 (A) LENGTH: 2051 base pairs

97 (B) TYPE: nucleic acid

98 (C) STRANDEDNESS: single

99 (D) TOPOLOGY: linear

101 (vii) IMMEDIATE SOURCE:

102 (A) LIBRARY: MUSCNOT07

103 (B) CLONE: 3014759

105 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

107	TCAGTTTCCT	GCCAATGACG	CTGGGGCAGC	CGGGGCAGCC	GGGGCAGCCC	GGTCACCCCG	60
108	CCCCCAGGCC	CACACTAAGG	GTGTCCGCGG	CCTGCCCTCC	AGGCGGAGGA	GCCCCGACTG	120
109	CGGAAGGATG	GAGCTGGCCG	CCGGAAGCTT	CTCGGAGGAG	CAGTTCTGGG	AGGCCTGCGC	180
110	CGAGCTCCAG	CAGCCCGCTC	TGGCCGGGGC	CGACTGGCAG	CTCCTAGTGG	AGACCTCGGG	240
111	CATCAGCATC	TACCGGCTGC	TGGACAAGAA	GACTGGACTT	TATGAGTATA	AAGTCTTTGG	300
112	TGTTCTGGAG	GACTGCTCAC	CAACTCTACT	GGCAGACATC	TATATGGACT	CAGATTACAG	360
113	AAAACAATGG	GACCAGTATG	TTAAAGAACT	CTATGAACAA	GAATGCAACG	GAGAGACTGT	420
114	GGTCTACTGG	GAAGTGAAGT	ACCCTTTTCC	CATGTCCAAC	AGAGACTATG	TCTACCTTCG	480
115	GCAGCGGCGA	GACCTGGACA	TGGAAGGGAG	GAAGATCCAT	GTGATCCTGG	CCCGGAGCAC	540
116	CTCCATGCCT	CAGCTTGCGG	AGAGGTCTGG	GGTGATCCGG	GTGAAGCAAT	ACAAGCAGAG	600

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117 CCTGGCGATT GAGAGTGACG GCAAGAAGGG GAGCAAAGTT TTCATGTATT ACTTCGATAA 660
118 CCCGGGTGGC CAAATTCCGT CCTGGCTCAT TAACTGGGCC GCCAAGAATG GAGTTCCTAA 720
119 CTTCTTGAAA GACATGGCAA GAGCCTGTCA GAACTACCTC AAGAAAACCT AAGAAAGAGA 780
120 ACTGGGAACA TTGCATCCAT GGGTTGATGT CTCTGGAAGT GCAACCACCC AATGTCTCTG 840
121 GAAGTGCCAC CTGGAAGTGC CACCTGGAAG TGTCTCTGGA AGAGCACCCA CCACTGTTCA 900
122 GCCTTCCCCT GCTGTTTCTG TCTTCAGAGG CCTACACACT ACCACATCCT TTCTAAGCAT 960
123 GTTTCCTGA CATCCAGCTC ACTCGTCTGC TTCCTTTCTC GCTCCCCCCC ATCCTGGGGC 1020
124 TGGGGCTGCC TTCTTCTACA GTTCAATATG GGGCAGACTA GGGAAACCTT TGCTTGCTTA 1080
125 CTATTAGGAG GGGAAGTCTT CAGTAGGGAA CACGATCATT CCATTGTGCA ATTTTACGGG 1140
126 GATGGGTGGG CGGAGGGACA CAACAAAATT TAAGAATGAC TATTTGGGCG GGCTGGCTCT 1200
127 TTTGCAGCTT GTGATTTCTT CCAGCTTGGG AGGGGCTGCT GGAAGTGGCA TTTCGTTTCA 1260
128 AGCTGACTTT CAGTGCACCC AAAGTGGATG ACGTGCCAAT GTCCATTTGC CTTATGCTTT 1320
129 GTGGAGCTGA TTAGGCTGGG ATTTGAGGTG ATAATCCAGT AAGTCTTTCC TCGTTCCTAC 1380
130 TTGTGGAGGA TCAGTAGCTG TTATGATGCC AGACCATTTG GAGAAGTATC AGAGGCCTGA 1440
131 CCGGACACAT AATACGACAA CCACATTTTT CCTCATCATC CATGAGGAAA TGGATGATTT 1500
132 CTCTTTTCCA TATGTCACTG GGGGAAAGGC TGCCTGTACC TCTCAAGCTT TGCATTTTAC 1560
133 TGGAAACTGA GCGTCAAGA TGGCTGTGGC CAGCTAGCAA AAGCAAAGAT GCTTTGTGCA 1620
134 TAGCCTTGTG AAAAAGTATC TTTCTATGCA ATAAGATGAA TTTTCTCCC AGAATATTTA 1680
135 GAAATGTAGA AGGGATAACA GTTCACAGCC AGGTAAAATT TAACTGGTGG CTTAATGACT 1740
136 CTGCACCTTT TTCTCAGGAA TTCTGCCTAA GTTGTCTGCC TTTTCTACCA CCAAAAAGAC 1800
137 TTTTAGTTTT CTATGCTTTC TCCTGAATTT TGGTAGGGTA AGGTATTTCT ATGTCAAAGG 1860
138 CACAGCCTTG ATGATCTCAG GGAAAAATTT TAATCACTGT GTATAATGAT ACTGAACCTT 1920
139 GATTAATAAC AGAAATTCAG GATGTAAAGC CACAGAATGG GATTTATTAA TGTGGGATAC 1980
140 CTCAGACTGT TTGTTTTCTT TCTGGGAAGA AAAGTGTGTT CTATAATGAA TAAATATAGA 2040
141 GTGGTTTTTA A 2051
143 (2) INFORMATION FOR SEQ ID NO: 3:
145 (i) SEQUENCE CHARACTERISTICS:
146 (A) LENGTH: 227 amino acids
147 (B) TYPE: amino acid
148 (C) STRANDEDNESS: single
149 (D) TOPOLOGY: linear
151 (vii) IMMEDIATE SOURCE:
152 (A) LIBRARY: LUNGTUT12
153 (B) CLONE: 3126479
155 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
157 Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
158 1 5 10 15
159 Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
160 20 25 30
161 Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
162 35 40 45
163 Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
164 50 55 60
165 Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
166 65 70 75 80
167 Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
168 85 90 95
169 Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
170 100 105 110

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Output Set: N:\CRF4\01092003\I879401A.raw

```

171 Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Glu Gly Lys Ile
172      115      120      125
173 Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
174      130      135      140
175 Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
176      145      150      155      160
177 Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
178      165      170      175
179 Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
180      180      185      190
181 Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
182      195      200      205
184 Pro Arg Gly Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
185      210      215      220
186 Ala Ala Cys
187 225

```

189 (2) INFORMATION FOR SEQ ID NO: 4:

191 (i) SEQUENCE CHARACTERISTICS:

192 (A) LENGTH: 903 base pairs

193 (B) TYPE: nucleic acid

194 (C) STRANDEDNESS: single

195 (D) TOPOLOGY: linear

197 (vii) IMMEDIATE SOURCE:

198 (A) LIBRARY: LUNGTUT12

199 (B) CLONE: 3126479

201 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

203 AGTACTTGTG TCCGGGTGGT GGA CTGGATT CGCTGCGGAG CCCTGGAAGC TGCCTTTCCT      60
204 TCTCCCTGTG CTTAACCAGA GGTGCCCATG GGTTGGACAA TGAGGCTGGT CACAGCAGCA      120
205 CTGTTACTGG GTCTCATGAT GGTGGTCACT GGAGACGAGG ATGAGAACAG CCCGTGTGCC      180
206 CATGAGGCC TCTTGACGA GGACACCCTC TTTTGCCAGG GCCTTGAAGT TTTCTACCCA      240
207 GAGTTGGGGA ACATTGGCTG CAAGGTTGTT CCTGATTGTA ACAACTACAG ACAGAAGATC      300
208 ACCTCCTGGA TGGAGCCGAT AGTCAAGTTC CCGGGGGCCG TGGACGGCGC AACCTATATC      360
209 CTGGTGATGG TGGATCCAGA TGCCCCTAGC AGAGCAGAAC CCAGACAGAG ATTCTGGAGA      420
210 CATTGGCTGG TAACAGATAT CAAGGGCGCC GACCTGAAGG AAGGGAAGAT TCAGGGCCAG      480
211 GAGTTATCAG CCTACCAGGC TCCCTCCCA CCGGCACACA GTGGCTTCCA TCGCTACCAG      540
212 TTCTTTGTCT ATCTTCAGGA AGGAAAAGTC ATCTCTCTCC TTCCCAAGGA AAACAAAAC      600
213 CGAGGCTCTT GGAAATGGA CAGATTTCTG AACCCTTCC ACCTGGGCGA ACCTGAAGCA      660
214 AGCACCCAGT TCATGACCCA GAACTACCAG GACTCACCAA CCCTCCAGGC TCCCAGAGGA      720
215 AGGGCCAGCG AGCCCAAGCA CAAAACCAG GCGGAGATAG CTGCCTGCTA GATAGCCGGC      780
216 TTTGCCATCC GGGCATGTGG CCACACTGCC CACCACCGAC GATGTGGGTA TGGAACCCCC      840
217 TCTGGATACA GAACCCTTC TTTTCCAAAT AAAAAAAAAA TCATCCAGGG CTTGGTGCTT      900
218 TGT
219
220 (2) INFORMATION FOR SEQ ID NO: 5:
221
222 (i) SEQUENCE CHARACTERISTICS:
223 (A) LENGTH: 213 amino acids
224 (B) TYPE: amino acid
225 (C) STRANDEDNESS: single
226 (D) TOPOLOGY: linear
227
228 (vii) IMMEDIATE SOURCE:

```

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Input Set : N:\CrF3\RULE60\09879401.raw.txt

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229 (A) LIBRARY: GenBank  
 230 (B) CLONE: 897693  
 232 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 234 Met Asp Pro Gly Ala Gly Ala Phe Ser Glu Glu Gln Phe Arg Glu Ala  
 235 1 5 10 15  
 236 Cys Ala Glu Leu Gln Arg Pro Ala Leu Ser Gly Ala Ala Trp Glu Leu  
 237 20 25 30  
 238 Leu Val Glu Thr Gln Gly Ile Ser Val Tyr Arg Leu Leu Asp Gln Gln  
 239 35 40 45  
 240 Thr Gly Leu Tyr Ala Tyr Lys Val Phe Gly Val Leu Glu Asp Cys Leu  
 241 50 55 60  
 242 Pro Asp Leu Leu Ala Asp Val Tyr Met Asp Leu Ala Tyr Arg Lys Gln  
 243 65 70 75 80  
 245 Trp Asp Gln Tyr Val Lys Glu Leu Tyr Glu Lys Glu Cys Ser Gly Glu  
 246 85 90 95  
 247 Thr Val Val Tyr Trp Gln Val Lys Tyr Pro Phe Pro Met Ser Asn Arg  
 248 100 105 110  
 249 Asp Tyr Val Tyr Val Arg Gln Arg Gln Glu Leu Asp Phe Glu Gly Gln  
 250 115 120 125  
 251 Lys Val His Val Ile Leu Ala Gln Ser Thr Ser Glu Pro Gln Phe Pro  
 252 130 135 140  
 253 Glu Lys Ser Gly Val Ile Arg Val Lys His Tyr Lys Gln Arg Leu Ala  
 254 145 150 155 160  
 255 Ile Gln Ser Asp Gly Lys Lys Gly Ser Lys Val Phe Met Tyr Tyr Phe  
 256 165 170 175  
 257 Asp Asn Pro Gly Gly Gln Ile Pro Ser Trp Val Ile Asn Trp Ala Ala  
 258 180 185 190  
 259 Lys Asn Gly Val Pro Asn Phe Leu Lys Asp Met Val Lys Ala Cys Gln  
 260 195 200 205  
 261 Asn Tyr Lys Lys Thr  
 262 210  
 264 (2) INFORMATION FOR SEQ ID NO: 6:  
 266 (i) SEQUENCE CHARACTERISTICS:  
 267 (A) LENGTH: 152 amino acids  
 268 (B) TYPE: amino acid  
 269 (C) STRANDEDNESS: single  
 270 (D) TOPOLOGY: linear  
 272 (vii) IMMEDIATE SOURCE:  
 273 (A) LIBRARY: GenBank  
 274 (B) CLONE: 1143527  
 276 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 278 Val Val Ser Thr Ser Pro Thr Lys Leu Val Asn Val Ser Tyr Asn Asn  
 279 1 5 10 15  
 280 Leu Thr Val Asn Leu Gly Asn Glu Leu Thr Pro Thr Gln Val Lys Asn  
 281 20 25 30  
 282 Gln Pro Thr Lys Val Ser Trp Asp Ala Glu Pro Gly Ala Leu Tyr Thr  
 283 35 40 45  
 284 Leu Val Met Thr Asp Pro Asp Ala Pro Ser Arg Lys Asn Pro Val Phe  
 285 50 55 60

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/879,401A

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Input Set : N:\Crf3\RULE60\09879401.raw.txt

Output Set: N:\CRF4\01092003\I879401A.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]